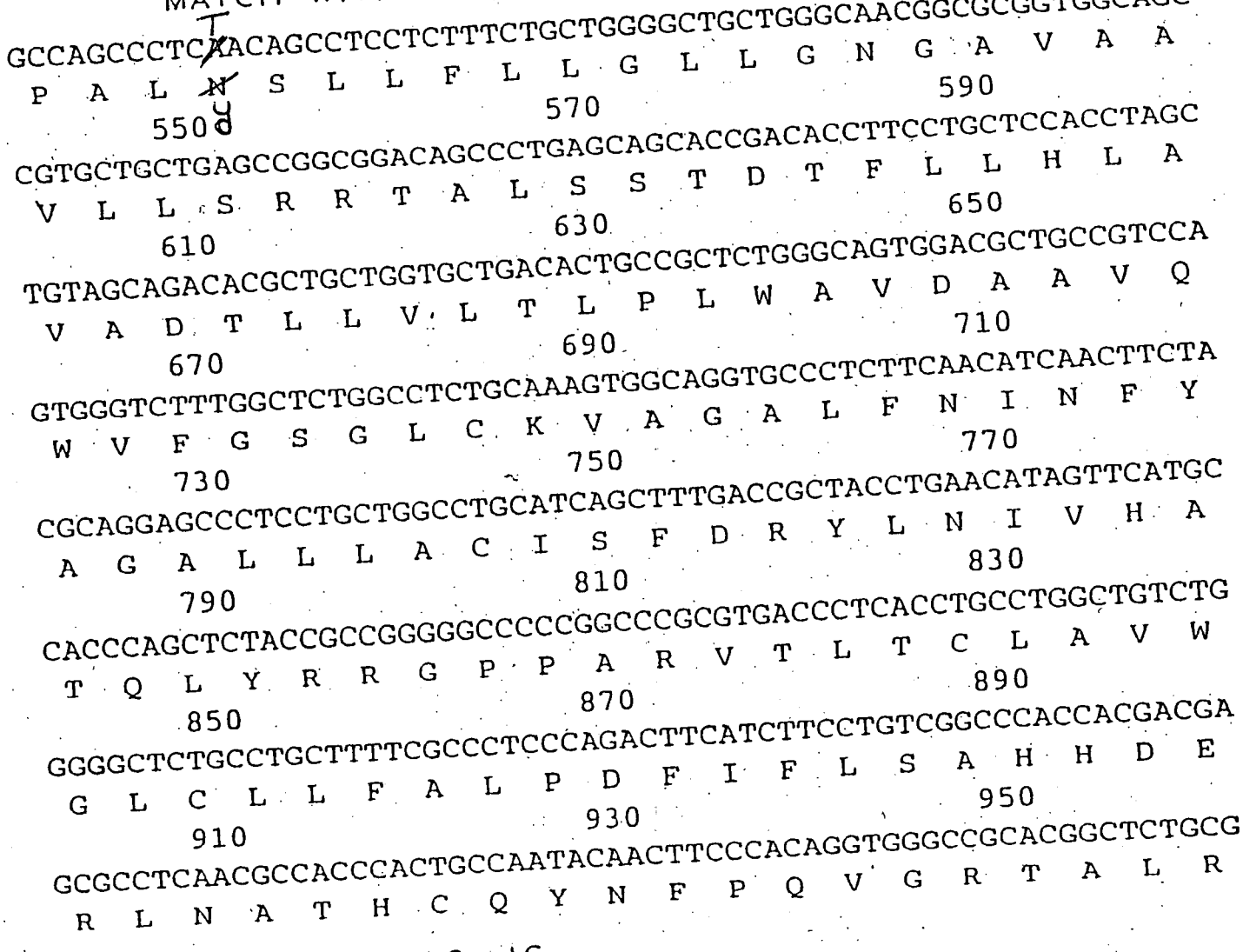
FIG. 1A

```
        10                  30                  50
CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG
        70                  90                  110
GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG
       130                 150                 170
AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT
                                                    M   E   L
       190                 210                 230
GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA
 R   K   Y   G   P   G   R   L   A   G   T   V   I   G   G   A   A   Q   S   K
       250                 270                 290
ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC
 S   Q   T   K   S   D   S   I   T   K   E   F   L   P   G   L   Y   T   A   P
       310                 330                 350
TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT
 S   S   P   F   P   P   S   Q   V   S   D   H   Q   V   L   N   D   A   E   V
       370                 390                 410
TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC
 A   A   L   L   E   N   F   S   S   S   Y   D   Y   G   E   N   E   S   D   S
       430                 450                 470
GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT
 C   C   T   S   P   P   C   P   Q   D   F   S   L   N   F   D   R   A   F   L
       490                 510                 530
```

MATCH WITH FIG. 1B

MATCH WITH FIG. IA

FIG. IB



MATCH WITH FIG. IC

MATCH WITH FIG. 1B

FIG. 1C

```
      970                 990                1010
GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC
 V  L  Q  L  V  A  G  F  L  L  P  L  L  V  M  A  Y  C  Y  A
      1030                1050               1070
CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT
 H  I  L  A  V  L  L  V  S  R  G  Q  R  R  L  R  A  M  R  L
      1090                1110               1130
GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT
 V  V  V  V  V  V  A  F  A  L  C  W  T  P  Y  H  L  V  V  L
      1150                1170               1190
GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT
 V  D  I  L  M  D  L  G  A  L  A  R  N  C  G  R  E  S  R  V
      1210                1230               1250
AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT
 D  V  A  K  S  V  T  S  G  L  G  Y  M  H  C  C  L  N  P  L
      1270                1290               1310
GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT
 L  Y  A  F  V  G  V  K  F  R  E  R  M  W  M  L  L  L  R  L
```

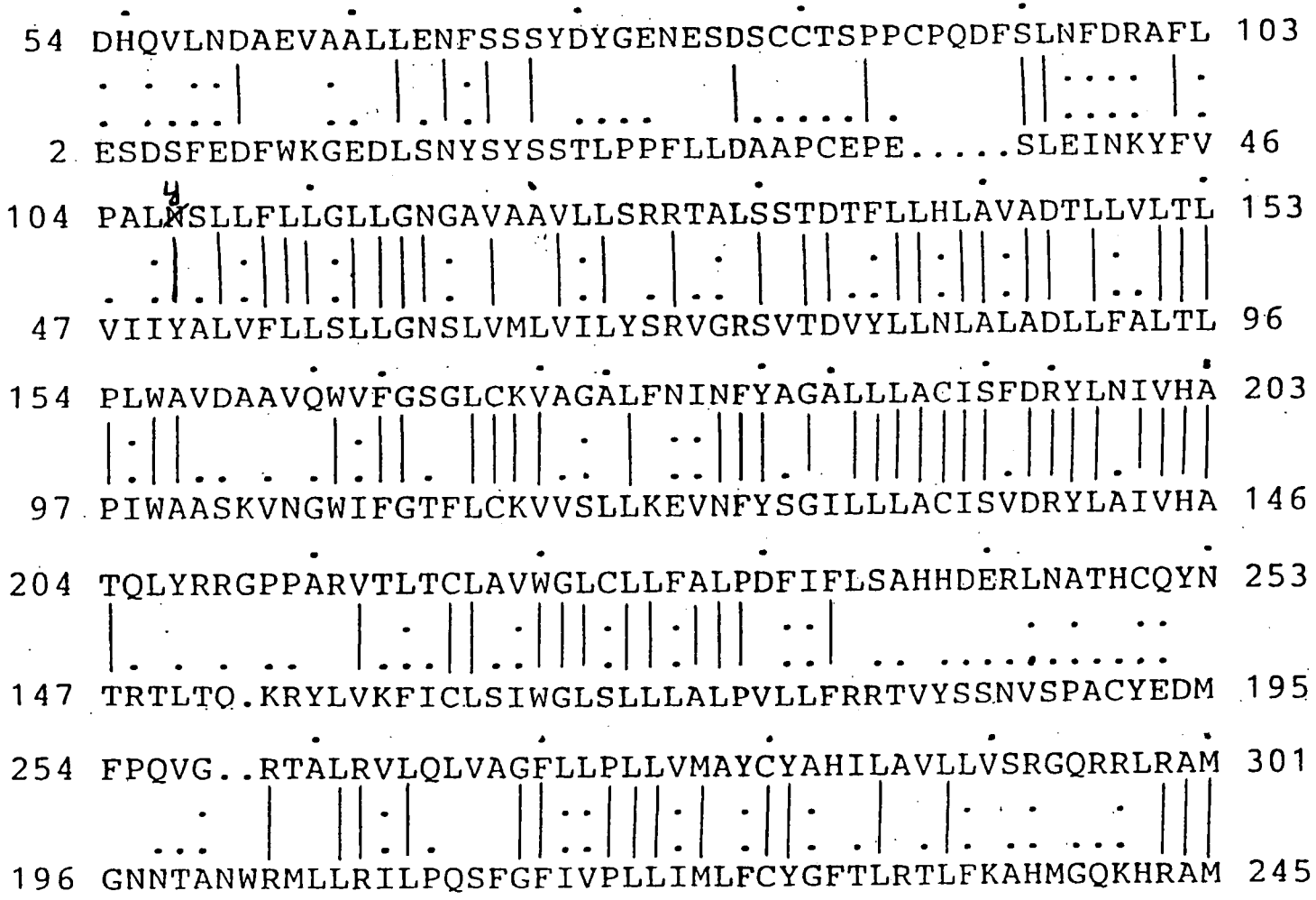
MATCH WITH FIG. 1D

MATCH WITH FIG. IC

FIG. ID

```
      1330                 1350                 1370
GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC
 G   C   P   N   Q   R   G   L   Q   R   Q   P   S   S   S   R   R   D   S   S
      1390                 1410                 1430
CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC
 W   S   E   T   S   E   A   S   Y   S   G   L   *
      1450                 1470                 1490
TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG
      1510                 1530                 1550
CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC
      1570                 1590                 1610
GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC
      1630                 1650                 1670
CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA
      1690                 1710                 1730
ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA
      1750                 1770                 1790
AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT
      1810                 1830                 1850
ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG
      1870
TCAGGAAAAAAAAAAA
```

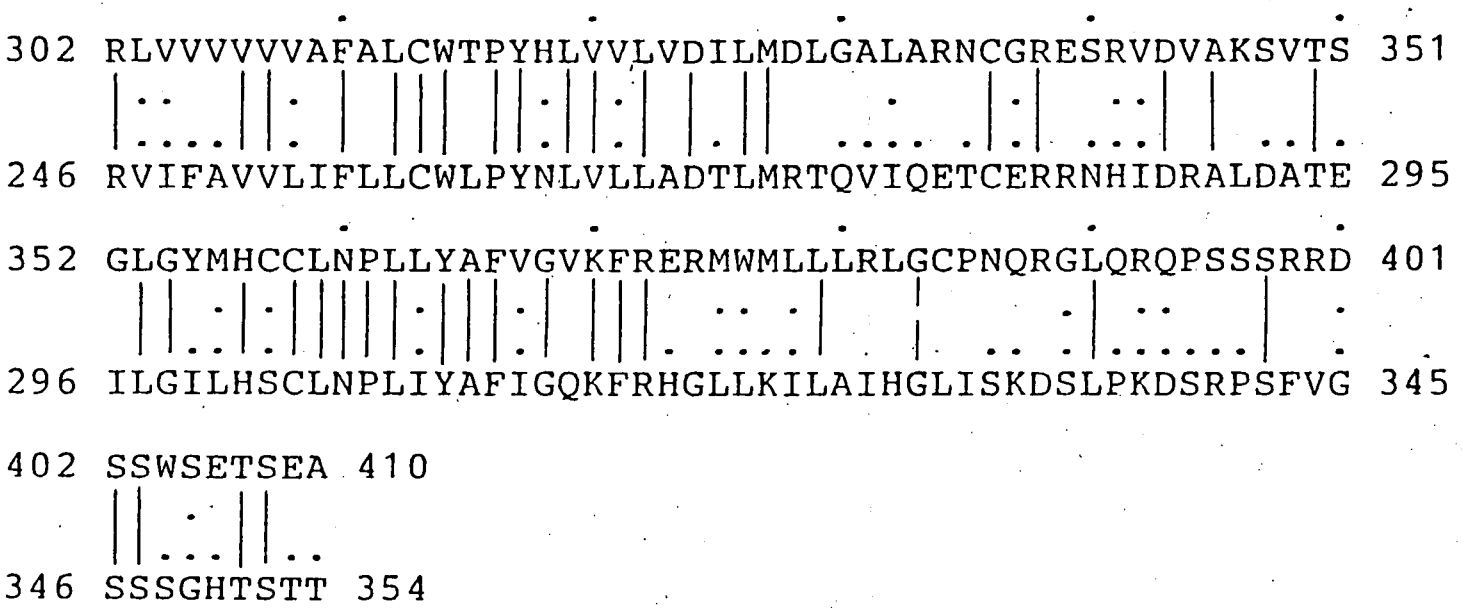
FIG. 2A



MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

FIG. 2B



VIA HAND DELIVERY MARCH 18, 2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

SUBMISSION OF SUBSTITUTE FORMAL DRAWINGS

Commissioner for Patents
Washington, D.C. 20231

To the Official Draftsperson:

Applicants submit herewith Substitute Formal Drawings of Figures 1A-1D and 2A-2B (six sheets) to replace the previously filed drawings of Figures 1A-1D and 2A-2B (six sheets). The enclosed drawings have been amended to correspond to the sequences shown in the Substitute Sequence Listing filed herewith, as discussed in detail in the Response and Amendment also filed herewith.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: March 18, 2002

Mark J. Hyman (Reg. No. 46,789)
Attorney for Applicants

Human Genome Sciences, Inc.
9410 Key West Avenue
Rockville, MD 20850
(240) 314-1224

Enclosures
KKH/MJH/KC/mlm

FIG. 1A

```
        10                  30                  50
CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG
        70                  90                 110
GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG
       130                 150                 170
AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT
                                                  M   E   L
       190                 210                 230
GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA
 R   K   Y   G   P   G   R   L   A   G   T   V   I   G   G   A   A   Q   S   K
       250                 270                 290
ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC
 S   Q   T   K   S   D   S   I   T   K   E   F   L   P   G   L   Y   T   A   P
       310                 330                 350
TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT
 S   S   P   F   P   P   S   Q   V   S   D   H   Q   V   L   N   D   A   E   V
       370                 390                 410
TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC
 A   A   L   L   E   N   F   S   S   S   Y   D   Y   G   E   N   E   S   D   S
       430                 450                 470
GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT
 C   C   T   S   P   P   C   P   Q   D   F   S   L   N   F   D   R   A   F   L
```

FIG. 1B

```
       490                   510                   530
GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC
 P  A  L  Y  S  L  L  F  L  L  G  L  L  G  N  G  A  V  A  A
       550                   570                   590
CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC
 V  L  L  S  R  R  T  A  L  S  S  T  D  T  F  L  L  H  L  A
       610                   630                   650
TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA
 V  A  D  T  L  L  V  L  T  L  P  L  W  A  V  D  A  A  V  Q
       670                   690                   710
GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA
 W  V  F  G  S  G  L  C  K  V  A  G  A  L  F  N  I  N  F  Y
       730                   750                   770
CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC
 A  G  A  L  L  L  A  C  I  S  F  D  R  Y  L  N  I  V  H  A
       790                   810                   830
CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG
 T  Q  L  Y  R  R  G  P  P  A  R  V  T  L  T  C  L  A  V  W
       850                   870                   890
GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA
 G  L  C  L  L  F  A  L  P  D  F  I  F  L  S  A  H  H  D  E
```

FIG. 1C

```
      910                 930                 950
GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG
 R  L  N  A  T  H  C  Q  Y  N  F  P  Q  V  G  R  T  A  L  R
      970                 990                1010
GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC
 V  L  Q  L  V  A  G  F  L  L  P  L  L  V  M  A  Y  C  Y  A
     1030                1050                1070
CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT
 H  I  L  A  V  L  L  V  S  R  G  Q  R  R  L  R  A  M  R  L
     1090                1110                1130
GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT
 V  V  V  V  V  V  A  F  A  L  C  W  T  P  Y  H  L  V  V  L
     1150                1170                1190
GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT
 V  D  I  L  M  D  L  G  A  L  A  R  N  C  G  R  E  S  R  V
     1210                1230                1250
AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT
 D  V  A  K  S  V  T  S  G  L  G  Y  M  H  C  C  L  N  P  L
     1270                1290                1310
GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT
 L  Y  A  F  V  G  V  K  F  R  E  R  M  W  M  L  L  L  R  L
```

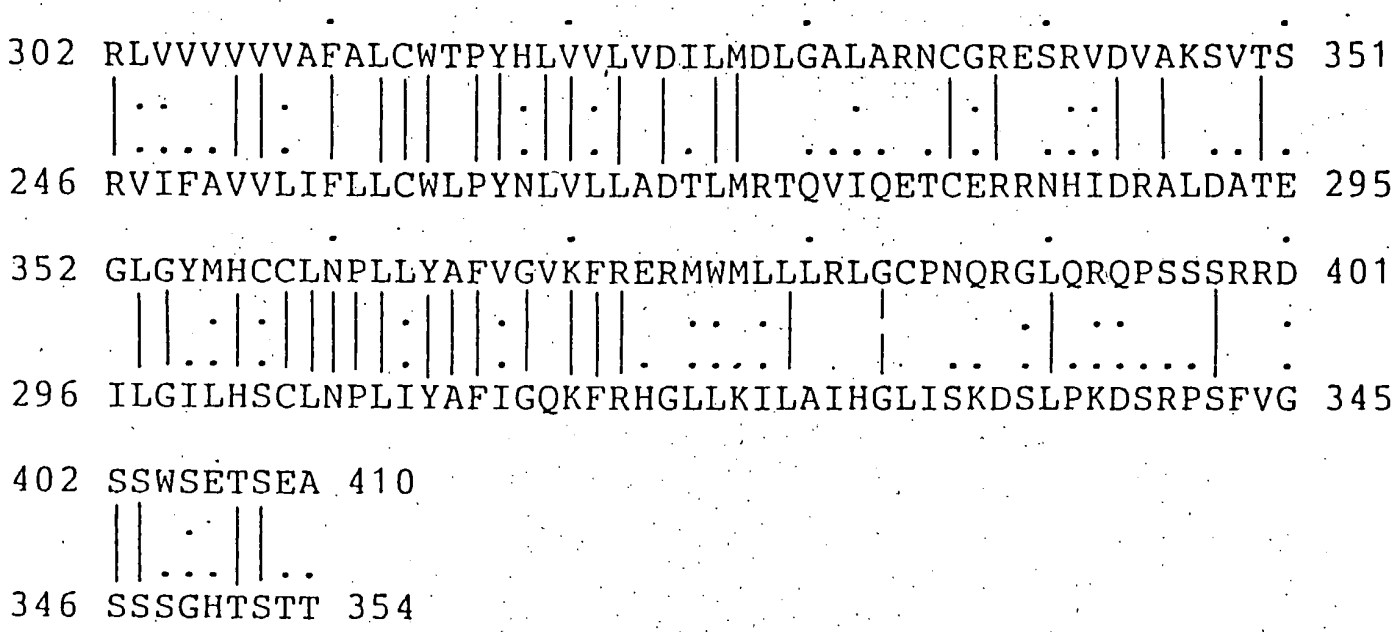
FIG. 1D

```
      1330                 1350                 1370
GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC
 G   C   P   N   Q   R   G   L   Q   R   Q   P   S   S   S   R   R   D   S   S
      1390                 1410                 1430
CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC
 W   S   E   T   S   E   A   S   Y   S   G   L   *
      1450                 1470                 1490
TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG
      1510                 1530                 1550
CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC
      1570                 1590                 1610
GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC
      1630                 1650                 1670
CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA
      1690                 1710                 1730
ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA
      1750                 1770                 1790
AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT
      1810                 1830                 1850
ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG
      1870
TCAGGAAAAAAAAAAA
```

FIG. 2A


54 DHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFL 103
2 ESDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPCEPE.....SLEINKYFV 46
104 PALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTL 153
47 VIIYALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTL 96
154 PLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHA 203
97 PIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHA 146
204 TQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYN 253
147 TRTLTQ.KRYLVKFICLSIWGLSLLLALPVLLFRRTVYSSNVSPACYEDM 195
254 FPQVG..RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAM 301
196 GNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQKHRAM 245

FIG. 2B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246 RVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE 295
352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRD 401
296 ILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVG 345
402 SSWSETSEA 410
346 SSSGHTSTT 354

VIA HAND DELIVERY MARCH 18, 2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

STATEMENT UNDER 37 C.F.R. §§1.821 AND 1.825

Commissioner for Patents
Washington, D.C. 20231

Sir:

Pursuant to 37 C.F.R. §§1.821(f) and 1.825(b), Applicants hereby certify that the sequence listing information recorded in computer readable form and submitted herewith is identical to the written (on paper) Substitute Sequence Listing submitted herewith.

Applicants further certify under 37 C.F.R. §§1.821(g) and 1.825(a) that the Substitute Sequence Listing submitted herewith contains no new matter.

Respectfully submitted,

Dated: March 18, 2002

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Enclosures
KKH/MJH/KC

SEQUENCE LISTING

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<120> Human G-Protein Chemokine Receptor HSATU68

<130> PF218US

<140> US 09/101,518
<141> 1998-12-21

<150> PCT/US96/00499
<151> 1996-01-11

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agaagcagcc tttgagaagg gaagtcacta tcccagagcc cagactgagc gg atg gag    178
                                                          Met Glu
                                                          1

ttg agg aag tac ggc cct gga aga ctg gcg ggg aca gtt ata gga gga      226
Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile Gly Gly
        5                  10                  15

gct gct cag agt aaa tca cag act aaa tca gac tca atc aca aaa gag      274
Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr Lys Glu
    20                  25                  30

ttc ctg cca ggc ctt tac aca gcc cct tcc tcc ccg ttc ccg ccc tca      322
Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro Pro Ser
35                  40                  45                  50

cag gtg agt gac cac caa gtg cta aat gac gcc gag gtt gcc gcc ctc      370
Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala Ala Leu
                55                  60                  65

ctg gag aac ttc agc tct tcc tat gac tat gga gaa aac gag agt gac      418
Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu Ser Asp
            70                  75                  80
```

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tcg tgc tgt acc tcc ccg ccc tgc cca cag gac ttc agc ctg aac ttc      466
Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu Asn Phe
        85                  90                  95

gac cgg gcc ttc ctg cca gcc ctc tac agc ctc ctc ttt ctg ctg ggg      514
Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu Leu Gly
    100                 105                 110

ctg ctg ggc aac ggc gcg gtg gca gcc gtg ctg ctg agc cgg cgg aca      562
Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg Arg Thr
115                 120                 125                 130

gcc ctg agc agc acc gac acc ttc ctg ctc cac cta gct gta gca gac      610
Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val Ala Asp
                135                 140                 145

acg ctg ctg gtg ctg aca ctg ccg ctc tgg gca gtg gac gct gcc gtc      658
Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala Ala Val
            150                 155                 160

cag tgg gtc ttt ggc tct ggc ctc tgc aaa gtg gca ggt gcc ctc ttc      706
Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala Leu Phe
        165                 170                 175

aac atc aac ttc tac gca gga gcc ctc ctg ctg gcc tgc atc agc ttt      754
Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile Ser Phe
    180                 185                 190

gac cgc tac ctg aac ata gtt cat gcc acc cag ctc tac cgc cgg ggg      802
Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg Arg Gly
195                 200                 205                 210

ccc ccg gcc cgc gtg acc ctc acc tgc ctg gct gtc tgg ggg ctc tgc      850
Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly Leu Cys
                215                 220                 225

ctg ctt ttc gcc ctc cca gac ttc atc ttc ctg tcg gcc cac cac gac      898
Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His His Asp
            230                 235                 240

gag cgc ctc aac gcc acc cac tgc caa tac aac ttc cca cag gtg ggc      946
Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln Val Gly
        245                 250                 255

cgc acg gct ctg cgg gtg ctg cag ctg gtg gct ggc ttt ctg ctg ccc      994
Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu Leu Pro
    260                 265                 270

ctg ctg gtc atg gcc tac tgc tat gcc cac atc ctg gcc gtg ctg ctg     1042
Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val Leu Leu
275                 280                 285                 290

gtt tcc agg ggc cag cgg cgc ctg cgg gcc atg cgg ctg gtg gtg gtg     1090
Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val Val Val
                295                 300                 305

gtc gtg gtg gcc ttt gcc ctc tgc tgg acc ccc tat cac ctg gtg gtg     1138
Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu Val Val
            310                 315                 320
```

Cont.

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ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc aac tgt ggc     1186
Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn Cys Gly
        325                 330                 335

cga gaa agc agg gta gac gtg gcc aag tcg gtc acc tca ggc ctg ggc     1234
Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly Leu Gly
    340                 345                 350

tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt gta ggg gtc     1282
Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val Gly Val
355                 360                 365                 370

aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg ggc tgc ccc     1330
Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly Cys Pro
                375                 380                 385

aac cag aga ggg ctc cag agg cag cca tcg tct tcc cgc cgg gat tca     1378
Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg Asp Ser
            390                 395                 400

tcc tgg tct gag acc tca gag gcc tcc tac tcg ggc ttg tga             1420
Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
        405                 410                 415

ggccggaatc cgggctcccc tttcgcccac agtctgactt ccccgcattc caggctcctc   1480

cctccctctg ccggctctgg ctctccccaa tatcctcgct cccgggactc actggcagcc   1540

ccagcaccac caggtctccc gggaagccac cctcccagct ctgaggactg caccattgct   1600

gctccttagc tgccaagccc catcctgccg cccgaggtgg ctgcctggag ccccactgcc   1660

cttctcattt ggaaactaaa acttcatctt ccccaagtgc ggggagtaca aggcatggcg   1720

tagagggtgc tgccccatga agccacagcc caggcctcca gctcagcagt gactgtggcc   1780

atggtcccca agacctctat atttggtctt ttatttttat gtctaaaatc ctgcttaaaa   1840

cttttcaata aacaagatcg tcaggaaaaa aaaaaa                              1876
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1               5                   10                  15

Gly Gly Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr
            20                  25                  30

Lys Glu Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro
        35                  40                  45
```

```
Pro Ser Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala
    50                  55                  60

Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu
65                  70                  75                  80

Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu
                85                  90                  95

Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu
            100                 105                 110

Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg
        115                 120                 125

Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val
    130                 135                 140

Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala
145                 150                 155                 160

Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala
                165                 170                 175

Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile
            180                 185                 190

Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg
        195                 200                 205

Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly
    210                 215                 220

Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His
225                 230                 235                 240

His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln
                245                 250                 255

Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu
            260                 265                 270

Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val
        275                 280                 285
```

Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val
290 295 300

Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu
305 310 315 320

Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn
325 330 335

Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly
340 345 350

Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val
355 360 365

Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly
370 375 380

Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg
385 390 395 400

Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
405 410 415

<210> 3
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Contains a BamHI restriction enzyme site

<400> 3
cgggatcctc catggagttg aggaagtac 29

<210> 4
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Contains complementary sequences to a BamHI site

<400> 4
ggcggatccc gctcacaagc ccgagtagga 30

<210> 5
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Contains a HindIII site

<400> 5
gtccaagctt gccaccatgg agttgaggaa gtac 34

<210> 6
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Contains complementary sequences to a XhoI site, translation stop codon, and an HA tag

<400> 6
ctgctcgagt caagcgtagt ctgggacgtc gtatgggtag cacaagcccg agtagga 57

<210> 7
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Contains a BamHI restriction enzyme site followed by 5 nucleotides resembling an efficient signal for the initiation of translation in eukaryotic cells (J. Mol. Biol. 1987, 196, 947-950, Kozak, M.)

D2 cont.

<400> 7
cgggatccct cccatggagt tgaggaagta c 31

<210> 8
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Contains the cleavage site for the restriction endonuclease BamHI

<400> 8
cgggatcccg ctcacaagcc cgagtagga 29

<210> 9
<211> 353
<212> PRT
<213> Homo sapiens

<400> 9

Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser Asn
1 5 10 15

Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala Pro
20 25 30

Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile Ile
35 40 45

Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met
50 55 60

Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr
65 70 75 80

Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro
85 90 95

Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu
100 105 110

Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile
115 120 125

D^2 cont.

Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His
130 135 140

Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile Cys
145 150 155 160

Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu Leu
165 170 175

Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr Glu
180 185 190

Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile Leu
195 200 205

Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe Cys
210 215 220

Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys
225 230 235 240

His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu
245 250 255

```
Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg
            260                 265                 270

Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp Arg
        275                 280                 285

Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu Asn
    290                 295                 300

Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu Leu
305                 310                 315                 320

Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro Lys
                325                 330                 335

Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser Thr
            340                 345                 350

Thr
```

D^2 cord.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Li | Attorney Docket No.: PF218US

Application Serial No.: 09/101,518 | Art Unit: 1646

Filed: January 11, 1996 | Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

DECLARATION OF MELANIE LENHART UNDER 37 C.F.R. § 1.132

I, Melanie Lenhart, hereby declare and state as follows:

1. I am employed by Human Genome Sciences, Inc. ("HGS"), Rockville, Maryland, as a Manager in the PreClinical Discovery department. Since I began working at HGS in 1995, my duties have primarily included carrying out and analyzing, as both a bench scientist and a manager, extensive DNA sequencing.

2. A partially redacted copy of the American Type Culture Collection ("ATCC") deposit receipt for Deposit Number 97334 is attached hereto as Exhibit A. As the deposit receipt indicates, ATCC Deposit Number 97334 contains a DNA plasmid assigned to the HGS Code Number 498,333, also known within HGS as HGS Clone ID HSATU68. I requested from the ATCC a sample of ATCC Deposit Number 97334 by a purchase order numbered 81449 dated March 13, 2001, a copy of which is attached hereto as Exhibit B. I received the sample of ATCC Deposit Number 97334 from the ATCC in April of 2001, as evidenced by Sales Order # S0241638 from the ATCC, a copy of which is attached hereto as Exhibit C.

3. I have been shown what has been presented to me as Figures 1A-1D as originally filed in the above-captioned patent application (hereinafter "original Figures

1A-1D"), a copy of which original Figures 1A-1D is attached hereto as Exhibit D. I used the nucleotide sequence of HSATU68, as shown in original Figures 1A-1D, as a reference to compare to the nucleotide sequence of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334.

4. A sample of ATCC Deposit Number 97334 was thoroughly sequenced under my supervision in my laboratory at HGS using sequencing methods which were routine and well known in the art prior to January 11, 1996. Exhibit E depicts an alignment of the nucleotide sequence of the deposited clone with the nucleotide sequence shown in original Figures 1A-1D.

5. The nucleotide sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at position 491. More particularly, original Figures 1A-1D show an A residue at position 491, while a T residue is present in the sequence obtained from the DNA clone contained in ATCC Deposit Number 97334.

6. As a result of the above difference at position 491 of the nucleotide sequence, the encoded amino acid sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at the 107^{th} codon. More particularly, the 107^{th} codon of the nucleotide sequence in original Figures 1A-1D shows an AAC, encoding for an Asn, which differs from the TAC sequence, encoding for a Tyr, deduced from the DNA clone contained in ATCC Deposit Number 97334.

7. The differences in the nucleotide and encoded amino acid sequences noted in paragraphs 5-6 above have been adjusted in the version of Figures 1A-1D attached hereto as Exhibit F. Exhibit G is a marked up version of original Figures 1A-1D showing in red ink the changes made. The nucleotide sequence shown in Exhibit G is identical at

all but one nucleotide to that shown in original Figures 1A-1D; the amino acid sequence shown in Exhibit F is identical at all but one amino acid residue to that shown in original Figures 1A-1D, with the same start codon, stop codon, and length.

8. Based on the experiments described above and the high degree of similarity between the nucleotide and amino acid sequences of original Figures 1A-1D and the corresponding sequences of the deposited clone as shown in Exhibits E, it is my belief that a person of ordinary skill in the art, upon routine sequencing of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334 using methods well known in the art prior to January 11, 1996, would readily determine that the residue at position 491 is an A residue; and thus, the encoded amino acid at position 107 is Tyr, especially when using original Figures 1A-1D as a guide.

9. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application captioned above or any patent issuing thereupon.

Date: 3/14/02

Melanie Lenhart